

## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

**This Page Blank (uspto)**

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	55	31.2	72	4	US-09-328-352-6545	Sequence 6545, Ap	
2	55	31.2	471	3	US-09-106-464-2	Sequence 2, Appli	
3	53	30.1	277	4	US-09-134-000C-4173	Sequence 4173, Ap	
4	52	29.5	75	4	US-09-543-681A-7857	Sequence 7857, Ap	
5	51.5	29.3	1094	3	US-09-268-347-32	Sequence 32, Appl	
6	51	29.0	165	3	US-08-965-689A-3	Sequence 3, Appli	
7	51	29.0	185	3	US-09-359-967-3	Sequence 3, Appli	
8	51	29.0	185	4	US-09-338-092-1224	Sequence 1224, Ap	
9	51	29.0	165	4	US-09-949-016-6345	Sequence 6345, Ap	
10	51	29.0	166	2	US-08-918-723-4	Sequence 4, Appli	
11	51	29.0	166	2	US-09-237-507-4	Sequence 4, Appli	
12	51	29.0	176	4	US-09-949-016-8150	Sequence 8150, Ap	
13	51	29.0	238	4	US-09-377-285B-2	Sequence 2, Appli	
14	51	29.0	354	4	US-09-377-285B-4	Sequence 4, Appli	
15	51	29.0	354	4	US-09-377-285B-26	Sequence 26, Appl	
16	51	29.0	354	4	US-09-377-285B-36	Sequence 36, Appl	
17	51	29.0	366	4	US-09-377-285B-38	Sequence 38, Appl	
18	51	29.0	455	3	US-09-130-339-2	Sequence 2, Appli	
19	50	28.4	96	4	US-09-621-976-7575	Sequence 7575, Ap	
20	50	28.4	106	4	US-09-621-976-7576	Sequence 7576, Ap	
21	50	28.4	106	4	US-09-621-976-7577	Sequence 7577, Ap	
22	50	28.4	106	4	US-09-621-976-7578	Sequence 7578, Ap	
23	50	28.4	198	4	US-09-270-767-36571	Sequence 36571, A	
24	50	28.4	198	4	US-09-270-767-51788	Sequence 51788, A	
25	50	28.4	476	4	US-09-673-300-10	Sequence 10, Appl	
26	50	28.4	501	4	US-09-502-540-11195	Sequence 11195, A	
27	48.5	27.6	220	3	US-09-052-089A-4	Sequence 4, Appli	

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,464
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/055,554
; FILING DATE: 13-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Spector, Eric S.
; REGISTRATION NUMBER: 22495
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-1500
; TELEFAX: 703-415-1508
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-464-2

Query Match 31.2%; Score 55; DB 3; Length 471;
Best Local Similarity 37.5%; Pred. No. 7.9;
Matches 12; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 KNESTNATNTKQWRDETKGFRDEAKRFKNTA 32
Db 415 KREATAIKRYWASEETEGFRSRAKEYKEMA 446

RESULT 3
US-09-134-000C-4173
; Sequence 4173, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4173
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4173

Query Match 30.1%; Score 53; DB 4; Length 277;
Best Local Similarity 34.6%; Pred. No. 8.3;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 7 NATNTKQWRDETKGFRDEAKRFKNTA 32
Db 108 NEESTKEWQDTIKYQSESEKERKQSA 133

RESULT 4
US-09-543-681A-7857
; Sequence 7857, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
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; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7857
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7857

Query Match 29.5%; Score 52; DB 4; Length 75;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 NESSTNATNTKQWRDETKGF 21
Db 4 NSMSNSMTGTGVKWFDEGKGF 23

RESULT 5
US-09-268-347-32
; Sequence 32, Application US/09268347
; Patent No. 6335182
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
; FILE REFERENCE: 1038-860
; CURRENT APPLICATION NUMBER: US/09/268,347
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1094
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-32

Query Match 29.3%; Score 51.5; DB 3; Length 1094;
Best Local Similarity 37.5%; Pred. No. 68;
Matches 12; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 3 ESSSTNATNTKQWRDETKGFRDEAKRFKN-TAG 33
Db 365 ETVINAVNKAGWRIKTTGANNQAGQFETVTSG 396

RESULT 6
US-08-965-689A-3
; Sequence 3, Application US/08965689A
; Patent No. 6015702
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,689A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,750
; FILING DATE: September 23, 1997
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; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ENDANOT01
; CLONE: 2456290
US-08-965-689A-3

Query Match 29.0%; Score 51; DB 3; Length 165;
Best Local Similarity 38.5%; Pred. No. 8.9;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
Db 132 DESGANVDASKWRRDREQFYKIAKQ 157

RESULT 7
US-09-359-967-3
; Sequence 3, Application US/09359967
; Patent No. 6146624
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,689
; FILING DATE:
; APPLICATION NUMBER: 08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: ENDANOT01
; CLONE: 2456290
US-09-359-967-3

Query Match 29.0%; Score 51; DB 3; Length 165;
Best Local Similarity 38.5%; Pred. No. 8.9;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
Db 132 DESGANVDASKWRRDREQFYKIAKQ 157

RESULT 8
US-09-538-092-1224
; Sequence 1224, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqformatter Version 0.9
; SEQ ID NO 1224
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P56554
US-09-538-092-1224

Query Match 29.0%; Score 51; DB 4; Length 165;
Best Local Similarity 38.5%; Pred. No. 8.9;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
Db 132 DESGANVDASKWRRDREQFYKIAKQ 157

RESULT 9
US-09-949-016-6345
; Sequence 6345, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6345
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Human
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US-09-237507-4  
; Sequence 4, Application US/09237507  
; Patent No. 5952181  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti

ORGANISM: Human

APPLICANT: Lal, Preeti

US-09-949-016-8150

Query Match 29.0%; Score 51; DB 4; Length 176;  
Best Local Similarity 38.5%; Pred. No. 9.6;  
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNKQRDETKGFRDEAKR 27  
Db 143 DESGANVDASRWDRDREQFYKIAKQ 168

## RESULT 13

US-09-377-285B-2  
; Sequence 2, Application US/09377285B  
; Patent No. 6720175  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
; FILE REFERENCE: JHU1580-4  
; CURRENT APPLICATION NUMBER: US/09/377,285B  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 2  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-377-285B-2

Query Match 29.0%; Score 51; DB 4; Length 238;  
Best Local Similarity 33.3%; Pred. No. 14;  
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 7 NATNTKQWRDETKGFRDEAKR 27  
Db 204 STANVKQWKQQLAAYQEEAER 224

## RESULT 14

US-09-377-285B-4  
; Sequence 4, Application US/09377285B  
; Patent No. 6720175  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
; FILE REFERENCE: JHU1580-4  
; CURRENT APPLICATION NUMBER: US/09/377,285B  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494

; PRIOR FILING DATE: 1999-06-10  
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; PRIOR FILING DATE: 1998-08-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 4  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-377-285B-4

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Best Local Similarity 33.3%; Pred. No. 22;  
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 7 NATNTKQWRDETKGFRDEAKR 27  
Db 204 STANVKQWKQQLAAYQEEAER 224

## RESULT 15

US-09-377-285B-26  
; Sequence 26, Application US/09377285B  
; Patent No. 6720175  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
; FILE REFERENCE: JHU1580-4  
; CURRENT APPLICATION NUMBER: US/09/377,285B  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 26  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-377-285B-26

Query Match 29.0%; Score 51; DB 4; Length 354;  
Best Local Similarity 33.3%; Pred. No. 22;  
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 7 NATNTKQWRDETKGFRDEAKR 27  
Db 204 STANVKQWKQQLAAYQEEAER 224

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Job time : 43 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:31:07 ; Search time 138 Seconds  
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Title: US-10-633-808-1

Perfect score: 176

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Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	100.0	33	US-10-444-662-8	Sequence 8, Appli
2	176	100.0	33	US-10-633-808-1	Sequence 1, Appli
3	176	100.0	33	US-10-633-808-22	Sequence 22, Appli
4	176	100.0	33	US-10-633-808-23	Sequence 23, Appli
5	176	100.0	33	US-10-633-808-36	Sequence 36, Appli
6	176	100.0	40	US-10-633-808-16	Sequence 16, Appli
7	176	100.0	160	US-10-633-808-5	Sequence 5, Appli
8	176	100.0	309	US-10-633-808-6	Sequence 6, Appli
9	176	100.0	424	US-10-633-808-7	Sequence 7, Appli
10	176	100.0	573	US-10-633-808-4	Sequence 4, Appli
11	173	98.3	33	US-10-633-808-14	Sequence 14, Appli
12	173	98.3	33	US-10-633-808-15	Sequence 15, Appli
13	173	98.3	33	US-10-782-075-7	Sequence 7, Appli

14	172	97.7	33	15	US-10-633-808-25	Sequence 25, Appli
15	167	94.9	33	15	US-10-633-808-26	Sequence 26, Appli
16	167	94.9	33	15	US-10-633-808-27	Sequence 27, Appli
17	165	93.8	31	15	US-10-633-808-21	Sequence 21, Appli
18	165	93.8	33	15	US-10-633-808-17	Sequence 17, Appli
19	160	90.9	30	15	US-10-633-808-20	Sequence 20, Appli
20	156	88.6	29	15	US-10-633-808-19	Sequence 19, Appli
21	152	86.4	28	15	US-10-633-808-18	Sequence 18, Appli
22	150	85.2	28	15	US-10-633-808-24	Sequence 24, Appli
23	150	85.2	28	15	US-10-633-808-30	Sequence 30, Appli
24	147	83.5	27	15	US-10-633-808-35	Sequence 35, Appli
25	141	80.1	33	15	US-10-633-808-34	Sequence 34, Appli
26	134	76.1	25	15	US-10-633-808-28	Sequence 28, Appli
27	134	76.1	25	15	US-10-633-808-29	Sequence 29, Appli
28	121	68.8	22	15	US-10-633-808-32	Sequence 32, Appli
29	79	44.9	15	15	US-10-633-808-31	Sequence 31, Appli
30	56.5	32.1	3079	15	US-10-369-493-2024	Sequence 2024, Ap
31	56	31.8	154	15	US-10-425-114-67327	Sequence 67327, A
32	56	31.8	188	15	US-10-866-527-62	Sequence 60470, A
33	54.5	31.0	508	17	US-10-866-527-62	Sequence 62, Appli
34	54	30.7	888	16	US-10-437-963-118322	Sequence 118322,
35	53.5	30.4	154	16	US-10-437-963-105218	Sequence 105218,
36	53.5	30.4	275	15	US-10-424-599-226978	Sequence 226978,
37	53.5	30.4	350	15	US-10-425-114-65017	Sequence 65017, A
38	53	30.1	553	15	US-10-104-047-2655	Sequence 2655, Ap
39	52.5	29.8	234	15	US-10-369-493-11114	Sequence 11114, A
40	52	29.5	175	15	US-10-424-599-151075	Sequence 151075,
41	52	29.5	205	15	US-10-425-114-62679	Sequence 62679, A
42	51	29.0	79	16	US-10-767-701-45937	Sequence 45937, A
43	51	29.0	145	16	US-10-437-963-124570	Sequence 124570,
44	51	29.0	148	14	US-10-180-524-2	Sequence 2, Appli
45	51	29.0	165	14	US-10-157-669-17	Sequence 17, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-444-662-8  
; Sequence 8, Application US/10444662  
; Publication No. US20030220264A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Rozema, David  
; APPLICANT: Wolff, Jon  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Ekena, Kirk  
; APPLICANT: Hagstrom, James  
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction  
; FILE REFERENCE: Mirus.035.01  
; CURRENT APPLICATION NUMBER: US/10/444,662  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-444-662-8

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESTNATNTKQWRDETKGFRDEAKRFKNTAG 33

DB 1 KNESTNATNTKQWRDETKGFRDEAKRFKNTAG 33

##### RESULT 2

US-10-633-808-1  
; Sequence 1, Application US/10633808  
; Publication No. US20040029826A1

GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-1

*Current application*

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 3  
US-10-633-808-22  
Sequence 22, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-22

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 4  
US-10-633-808-23  
Sequence 23, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex

APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-23

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 5  
US-10-633-808-36  
Sequence 36, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 36  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-36

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 6  
US-10-633-808-16  
Sequence 16, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO

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; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-16

Query Match      100.0%; Score 176; DB 15; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.3e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
    |||||
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 7
US-10-633-808-5
; Sequence 5, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-5

Query Match      100.0%; Score 176; DB 15; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
    |||||
Db 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89

RESULT 8
US-10-633-808-6
; Sequence 6, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-4

Query Match      100.0%; Score 176; DB 15; Length 424;
Best Local Similarity 100.0%; Pred. No. 7e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
    |||||
Db 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89

RESULT 9
US-10-633-808-7
; Sequence 7, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-7

Query Match      100.0%; Score 176; DB 15; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.9e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
    |||||
Db 206 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 238

RESULT 10
US-10-633-808-4
; Sequence 4, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-4
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Query Match 100.0%; Score 176; DB 15; Length 573;  
Best Local Similarity 100.0%; Pred. No. 9.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 206 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 238  
|||||

RESULT 11  
US-10-633-808-14  
; Sequence 14, Application US/10633808  
; Publication No. US20040029826A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Wong, So  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Sokoloff, Alex  
; APPLICANT: Monahan, Sean  
; APPLICANT: Sebestyen, Magdolna  
; APPLICANT: Wolff, Jon  
; APPLICANT: Higgs, Lori  
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
; FILE REFERENCE: Mirus.014.06  
; CURRENT APPLICATION NUMBER: US/10/633,808  
; CURRENT FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-633-808-14

Query Match 98.3%; Score 173; DB 15; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.1e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 12  
US-10-633-808-15  
; Sequence 15, Application US/10633808  
; Publication No. US20040029826A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Wong, So  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Sokoloff, Alex  
; APPLICANT: Monahan, Sean  
; APPLICANT: Sebestyen, Magdolna  
; APPLICANT: Wolff, Jon  
; APPLICANT: Higgs, Lori  
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
; FILE REFERENCE: Mirus.014.06  
; CURRENT APPLICATION NUMBER: US/10/633,808  
; CURRENT FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-633-808-15

Query Match 98.3%; Score 173; DB 15; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.1e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 13  
US-10-782-075-7  
; Sequence 7, Application US/10782075  
; Publication No. US20040167090A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Monahan, Sean  
; APPLICANT: Budker, Vladimir  
; APPLICANT: Nader, Lisa  
; APPLICANT: Subbotin, Vladimir  
; APPLICANT: Wolff, Jon A  
; TITLE OF INVENTION: Covalent Modification of RNA for In Vitro and In Vivo Delivery  
; FILE REFERENCE: Mirus.030.16.6  
; CURRENT APPLICATION NUMBER: US/10/782,075  
; CURRENT FILING DATE: 2004-02-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-782-075-7

Query Match 98.3%; Score 173; DB 16; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.1e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 14  
US-10-633-808-25  
; Sequence 25, Application US/10633808  
; Publication No. US20040029826A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Wong, So  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Sokoloff, Alex  
; APPLICANT: Monahan, Sean  
; APPLICANT: Sebestyen, Magdolna  
; APPLICANT: Wolff, Jon  
; APPLICANT: Higgs, Lori  
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
; FILE REFERENCE: Mirus.014.06  
; CURRENT APPLICATION NUMBER: US/10/633,808  
; CURRENT FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-633-808-25

Query Match 97.7%; Score 172; DB 15; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.5e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 15  
US-10-633-808-26

```
; Sequence 26, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdalena
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-26

Query Match      94.9%; Score 167; DB 15; Length 33;
Best Local Similarity 90.9%; Pred. No. 7.4e-16;
Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33
       :|||||:|||||:|||||:|||||:|||||:
DB      1 RNESSTNATNTKQWRDETKGFRDEARRPNTAG 33
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Search completed: March 30, 2005, 14:41:09  
Job time : 139 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:14:33 ; Search time 170 Seconds  
(without alignments)  
75.077 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESTNATNTKQWRDETKGPRDEAKRFKNTAG 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	33	ADH51594	Bacteriop
2	176	100.0	33	ADJ46278	T7 p17 ro
3	176	100.0	33	ADJ46313	T7 phage
4	176	100.0	40	ADJ46293	T7 phage
5	176	100.0	160	ADJ46282	T7 p17 pr
6	176	100.0	309	ADJ46283	T7 p17 pr
7	176	100.0	424	ADJ46284	T7 p17 pr
8	176	100.0	573	ADJ46281	T7 phage
9	173	98.3	33	ADJ46292	T7 phage
10	173	98.3	33	ADJ46291	T7 phage
11	173	98.3	33	ADJ46293	Bacteriop
12	172	97.7	33	ADJ46302	T7 phage
13	170	96.6	33	ADJ46299	T7 phage
14	170	96.6	33	ADJ46300	T7 phage
15	167	94.9	33	ADJ46304	T7 phage
16	167	94.9	33	ADJ46303	T7 phage
17	165	93.8	31	ADJ46298	T7 phage
18	165	93.8	33	ADJ46294	T7 phage
19	160	90.9	30	ADJ46297	T7 phage
20	156	88.6	29	ADJ46296	T7 phage
21	152	86.4	28	ADJ46295	T7 phage
22	150	85.2	28	ADJ46301	T7 phage
23	150	85.2	28	ADJ46307	T7 phage
24	147	83.5	27	ADJ46312	T7 phage
25	141	80.1	33	ADJ46311	T7 phage

26	134	76.1	25	8	ADJ46305	Adj46305 T7 phage
27	134	76.1	25	8	ADJ46306	Adj46306 T7 phage
28	121	68.8	22	8	ADJ46309	Adj46309 T7 phage
29	79	44.9	15	8	ADJ46308	Adj46308 T7 phage
30	60	34.1	1460	3	AAG40077	Arabidops
31	60	34.1	1462	3	AAG40076	Arabidops
32	60	34.1	1518	3	AAG40075	Arabidops
33	60	34.1	1604	3	AAG31284	Arabidops
34	60	34.1	1606	3	AAG31283	Arabidops
35	60	34.1	1662	3	AAG31282	Arabidops
36	56.5	32.1	3079	8	ADN19371	Bacterial
37	56	31.8	90	3	AAG26831	Adj26831 Zea mays
38	56	31.8	90	3	AAG35425	Adj35425 Zea mays
39	56	31.8	109	3	AAG35424	Adj35424 Zea mays
40	56	31.8	109	3	AAG26830	Adj26830 Zea mays
41	56	31.8	169	3	AAG35423	Adj35423 Zea mays
42	55	31.2	72	6	ADA35258	Adj35258 Acinetoba
43	55	31.2	470	2	AAW47172	AAW47172 Glucosyl
44	55	31.2	470	2	AAW06274	AAW06274 Tomato de
45	55	31.2	471	2	AAW98009	AAW98009 Medium-ch

## ALIGNMENTS

### RESULT 1

ADH51594

ID ADH51594 standard; peptide; 33 AA.

AC ADH51594;

DT 25-MAR-2004 (first entry)

DE Bacteriophage T7 peptide related to reversible compound modification.

KW amine-containing compound; membrane lipid; maleic anhydride;

KW reversible modification; cross-linker; membrane activity;

KW positive charge; toxicity.

OS Enterobacteria phage T7.

PN US2003220264-A1.

PD 27-NOV-2003.

PF 23-MAY-2003; 2003US-00444662.

PR 24-MAY-2002; 2002US-0383298P.

PA (ROZE/) ROZEMA D B.

PA (WAKE/) WAKEFIELD D.

PA (WOLF/) WOLFF J A.

PA (EXEN/) EXENA K.

PA (HAGS/) HAGSTROM J E.

PI Rozema DB, Wakefield D, Wolff JA, Ekana K, Hagstrom JE;

DR WPI; 2004-097358/10.

XX Reversible modification of an amine-containing compound useful for delivering molecules to cells involves covalently attaching a substituted maleic anhydride to the amine.

PS Example 12; SEQ ID NO 8; 17pp; English.

XX This invention relates to a novel reversible modification of an amine-containing compound to alter interaction of the compound with membrane lipids which involves covalently attaching a substituted maleic anhydride to the amine. The invention is useful for reversible modification of an amine-containing compound for delivering molecules to cells and as cross-linkers. The modification of the compound inactivates its membrane activity, reduces its positive charge and toxicity and reverses its charge. The present sequence is that of a bacteriophage T7 peptide which

CC is related to the invention.

XX Sequence 33 AA;

Query Match 100.0%; Score 176; DB 8; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.1e-19;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

DB 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

RESULT 2

ADJ46278

ID ADJ46278 standard; peptide; 33 AA.

XX

AC ADJ46278;

XX 06-MAY-2004 (first entry)

XX T7 p17 rod domain peptide, SEQ ID 1.

XX Hepatocyte delivery; T7; p17 rod domain.

XX Enterobacteria phage T7.

XX WO2004013307-A2.

XX 12-FEB-2004.

XX 04-AUG-2003; 2003WO-US024516.

XX 05-AUG-2002; 2002US-0401167P.

XX 04-AUG-2003; 2003US-00633808.

XX (MIRU-) MIRUS CORP.

XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

XX Wakefield D, Sebestyen MG;

XX WPI; 2004-203636/19.

XX Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to compound.

XX Claim 12; Page 2; 56pp; English.

XX The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278).

XX Sequence 33 AA;

Query Match

Best Local Similarity 100.0%; Score 176; DB 8; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

DB 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

RESULT 3

ADJ46313

ID ADJ46313 standard; peptide; 33 AA.

XX

AC ADJ46313;

XX 06-MAY-2004 (first entry)

XX T7 phase p17 protein ligand-related peptide, SEQ ID 36.

XX Hepatocyte delivery; T7; p17 rod domain.

XX Enterobacteria phage T7.

XX Synthetic.

XX Key Location/Qualifiers

XX FT Misc-difference 1.33

XX /note= "All D-form residues"

XX WO2004013307-A2.

XX 12-FEB-2004.

XX 04-AUG-2003; 2003WO-US024516.

XX 05-AUG-2002; 2002US-0401167P.

XX 04-AUG-2003; 2003US-00633808.

XX (MIRU-) MIRUS CORP.

XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

XX Wakefield D, Sebestyen MG;

XX WPI; 2004-203636/19.

XX Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to compound.

XX Disclosure; Page 10; 56pp; English.

XX The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-ADJ46313 are synthetic peptides derived from the T7 phase p17 protein ligand, where ADJ46291-ADJ46301 have amino acid changes which do not disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid changes which do disrupt hepatocyte targeting.

XX Sequence 33 AA;

Query Match

Best Local Similarity 100.0%; Score 176; DB 8; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

DB 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

RESULT 4

ADJ46293

ID ADJ46293 standard; peptide; 40 AA.

XX ADJ46293;

XX 06-MAY-2004 (first entry)

XX T7 phase p17 protein ligand, SEQ ID 16.

XX Hepatocyte delivery; T7; p17 rod domain.

XX



OS Enterobacteria phage T7.  
 XX Synthetic.  
 XX WO2004013307-A2.  
 XX 12-FEB-2004.  
 XX 04-AUG-2003; 2003WO-US024516.  
 XX 05-AUG-2002; 2002US-0401167P.  
 XX 04-AUG-2003; 2003US-00633808.  
 XX (MIRU-) MIRUS CORP.  
 XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Luttke J, Higgs L;  
 XX Wakefield D, Sebestyen MG;  
 XX WPI; 2004-203636/19.  
 XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 XX compound.  
 XX Disclosure; Page 10; 56pp; English.  
 XX The present invention relates to a composition (I) for delivering a  
 XX therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
 XX compound. In (I), the compound comprises a drug (interferon). (I)  
 XX provides better hepatocyte specificity and potentially utilizes different  
 XX cellular internalization pathways which allows more flexibility in  
 XX designing delivery strategies and is useful for delivering therapeutic  
 XX cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 XX p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
 XX ADJ46313 are synthetic peptides derived from the T7 phage p17 protein  
 XX ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
 XX disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
 XX changes which do disrupt hepatocyte targeting.  
 XX Sequence 40 AA;  
 XX Query Match 100.0%; Score 176; DB 8; Length 40;  
 XX Best Local Similarity 100.0%; Pred. No. 9e-19;  
 XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 DB |||||  
 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 57 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 89  
 RESULT 6  
 ADJ46282  
 ID ADJ46282 standard; protein; 309 AA.  
 XX AC ADJ46283;  
 XX 06-MAY-2004 (first entry)  
 XX T7 p17 protein fragment 1-289, SEQ ID 6.  
 XX Hepatocyte delivery; T7; p17 rod domain.  
 XX Enterobacteria phage T7.  
 XX WO2004013307-A2.  
 XX 12-FEB-2004.  
 XX 04-AUG-2003; 2003WO-US024516.  
 XX 05-AUG-2002; 2002US-0401167P.  
 XX 04-AUG-2003; 2003US-00633808.  
 XX (MIRU-) MIRUS CORP.  
 XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Luttke J, Higgs L;  
 XX Wakefield D, Sebestyen MG;  
 XX WPI; 2004-203636/19.  
 XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 XX compound.  
 XX Example 3; Page 26; 56pp; English.  
 XX The present invention relates to a composition (I) for delivering a  
 XX therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
 XX compound. In (I), the compound comprises a drug (interferon). (I)  
 XX provides better hepatocyte specificity and potentially utilizes different  
 XX cellular internalization pathways which allows more flexibility in  
 XX designing delivery strategies and is useful for delivering therapeutic  
 XX cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 XX p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present  
 XX sequence is the predicted sequence of a fragment of the T7 p17 protein.  
 XX Sequence 160 AA;  
 XX Query Match 100.0%; Score 176; DB 8; Length 160;  
 XX Best Local Similarity 100.0%; Pred. No. 4.9e-18;  
 XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 DB |||||  
 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 57 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 89  
 RESULT 5  
 ADJ46282  
 ID ADJ46282 standard; protein; 160 AA.  
 XX AC ADJ46282;  
 XX 06-MAY-2004 (first entry)  
 XX T7 p17 protein fragment 150-289, SEQ ID 5.  
 XX Hepatocyte delivery; T7; p17 rod domain.  
 XX Enterobacteria phage T7.  
 XX WO2004013307-A2.  
 XX 12-FEB-2004.  
 XX 04-AUG-2003; 2003WO-US024516.  
 XX 05-AUG-2002; 2002US-0401167P.  
 XX 04-AUG-2003; 2003US-00633808.  
 XX (MIRU-) MIRUS CORP.

CC cellular internalization pathways which allows more flexibility in  
 CC designing delivery strategies and is useful for delivering therapeutic  
 CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present  
 CC sequence is the predicted sequence of a fragment of the T7 p17 protein.  
 XX  
 SQ Sequence 309 AA;

Query Match 100.0%; Score 176; DB 8; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 |||||  
 DB 206 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 238

RESULT 7  
 ADJ46284  
 ID ADJ46284 standard; protein; 424 AA.  
 XX  
 AC ADJ46284;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE T7 p17 protein fragment 150-553, SEQ ID 7.  
 XX  
 DE Hepatocyte delivery; T7; p17 rod domain.  
 KW Hepatocyte delivery; T7; p17 rod domain.  
 XX  
 OS Enterobacteria phage T7.  
 XX  
 PN WO2004013307-A2.  
 XX  
 PD 12-FEB-2004.  
 XX  
 PF 04-AUG-2003; 2003WO-US024516.  
 XX  
 PR 05-AUG-2002; 2002US-0401167P.  
 PR 04-AUG-2003; 2003US-00633808.  
 XX  
 PA (MIRU-) MIRUS CORP.  
 XX  
 PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
 PI Wakefield D, Sebestyen MG;  
 XX  
 DR WPI; 2004-203636/19.  
 XX

Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 compound.  
 Example 3; Page 26; 56pp; English.  
 The present invention relates to a composition (I) for delivering a  
 therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
 compound. In (I), the compound comprises a drug (interferon). (I)  
 provides better hepatocyte specificity and potentially utilizes different  
 cellular internalization pathways which allows more flexibility in  
 designing delivery strategies and is useful for delivering therapeutic  
 cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present  
 sequence is the predicted sequence of a fragment of the T7 p17 protein.

Query Match 100.0%; Score 176; DB 8; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 |||||  
 DB 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89

RESULT 9  
 ADJ46292  
 ID ADJ46292 standard; peptide; 33 AA.  
 XX  
 AC ADJ46292;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE T7 phage p17 protein ligand, SEQ ID 15.  
 XX  
 KW Hepatocyte delivery; T7; p17 rod domain.  
 XX  
 OS Enterobacteria phage T7.  
 XX  
 OS Synthetic.

Query Match 100.0%; Score 176; DB 8; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 |||||  
 DB 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89

RESULT 8

ADJ46281

ID ADJ46281 standard; protein; 573 AA.

XX

AC ADJ46281;

XX

DT 06-MAY-2004 (first entry)

XX

DE T7 p17 protein, SEQ ID 4.

XX

KW Hepatocyte delivery; T7; p17 rod domain.

XX

OS Enterobacteria phage T7.

XX

PN WO2004013307-A2.

XX

PD 12-FEB-2004.

XX

PF 04-AUG-2003; 2003WO-US024516.

XX

PR 05-AUG-2002; 2002US-0401167P.

PR 04-AUG-2003; 2003US-00633808.

XX

PA (MIRU-) MIRUS CORP.

XX

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
 PI Wakefield D, Sebestyen MG;

XX

DR WPI; 2004-203636/19.

XX

SQ Sequence 573 AA;

Query Match 100.0%; Score 176; DB 8; Length 573;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-17;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 |||||  
 DB 206 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 238

RESULT 9

ADJ46292

ID ADJ46292 standard; peptide; 33 AA.

XX

AC ADJ46292;

XX

DT 06-MAY-2004 (first entry)

XX

DE T7 phage p17 protein ligand, SEQ ID 15.

XX

KW Hepatocyte delivery; T7; p17 rod domain.

XX

OS Enterobacteria phage T7.

XX

OS Synthetic.

FH Key Location/Qualifiers  
 FT Misc-difference 15  
 XX /note= "Wild-type residue replaced with Lys"  
 XX WO2004013307-A2.  
 XX 12-FEB-2004.  
 XX 04-AUG-2003; 2003WO-US024516.  
 XX 05-AUG-2002; 2002US-0401167P.  
 PR 04-AUG-2003; 2003US-00633808.  
 XX (MIRU-) MIRUS CORP.  
 PA Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
 XX Wakefield D, Sebestyen MG;  
 PI WPI; 2004-203636/19.  
 DR Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 PI compound.  
 PS Disclosure; Page 10; 56pp; English.  
 XX The present invention relates to a composition (I) for delivering a  
 CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
 CC compound. In (I), the compound comprises a drug (interferon). (I)  
 CC provides better hepatocyte specificity and potentially utilizes different  
 CC cellular internalization pathways which allows more flexibility in  
 CC designing delivery strategies and is useful for delivering therapeutic  
 CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
 CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
 CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
 CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
 CC changes which do disrupt hepatocyte targeting.  
 XX Sequence 33 AA;  
 SQ  
 Query Match 98.3%; Score 173; DB 8; Length 33;  
 Best Local Similarity 97.0%; Pred. No. 2e-18;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 RESULT 10  
 ADJ46291  
 ID ADJ46291 standard; peptide; 33 AA.  
 XX ADJ46291;  
 AC  
 XX 06-MAY-2004 (first entry)  
 DT T7 phase p17 protein ligand, SEQ ID 14.  
 DE Hepatocyte delivery; T7; p17 rod domain.  
 KW Enterobacteria phage T7.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FT Misc-difference 26  
 FT /note= "Wild-type residue replaced with Arg"  
 XX WO2004013307-A2.  
 XX 12-FEB-2004.  
 XX

PF 04-AUG-2003; 2003WO-US024516.  
 XX 05-AUG-2002; 2002US-0401167P.  
 PR 04-AUG-2003; 2003US-00633808.  
 XX (MIRU-) MIRUS CORP.  
 PA Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
 XX Wakefield D, Sebestyen MG;  
 PI WPI; 2004-203636/19.  
 DR Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 PI compound.  
 PS Disclosure; Page 10; 56pp; English.  
 XX The present invention relates to a composition (I) for delivering a  
 CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
 CC compound. In (I), the compound comprises a drug (interferon). (I)  
 CC provides better hepatocyte specificity and potentially utilizes different  
 CC cellular internalization pathways which allows more flexibility in  
 CC designing delivery strategies and is useful for delivering therapeutic  
 CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
 CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
 CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
 CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
 CC changes which do disrupt hepatocyte targeting.  
 XX Sequence 33 AA;  
 SQ  
 Query Match 98.3%; Score 173; DB 8; Length 33;  
 Best Local Similarity 97.0%; Pred. No. 2e-18;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
 RESULT 11  
 ADJ46293  
 ID ADJ46293 standard; peptide; 33 AA.  
 XX ADJ46293;  
 AC  
 XX 18-NOV-2004 (first entry)  
 DT Bacteriophage T7 cholesterol modified cell targeting peptide MC1054.  
 DE Post-synthetic modification; nuclease; siRNA; microRNA; cell delivery;  
 KW small interfering RNA; cell targeting peptide; cholesterol.  
 XX Enterobacteria phage T7.  
 OS  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Lys modified with cholesterol chloroformate"  
 XX US2004167090-A1.  
 XX 26-AUG-2004.  
 XX 19-FEB-2004; 2004US-00782075.  
 XX 21-FEB-2003; 2003US-0448789P.  
 PR 18-MAR-2003; 2003US-0455724P.  
 XX (MONA/) MONAHAN S D.  
 PA (BUDK/) BUDKER V G.  
 PA (NADE/) NADER L.

PA (SUBB/) SUBBOTIN V.  
 PA (WOLF/) WOLFF J A.  
 PI Monahan SD, Budker VG, Nader L, Subbotin V, Wolff JA;  
 PI WPI; 2004-615051/59.  
 DR  
 XX  
 PT New composition for delivering an RNA to a mammalian cell having a post-  
 PT synthetically modified RNA, useful for delivering oligonucleotides and  
 PT small RNAs to cells in vitro and in vivo.  
 XX  
 XX Example 15; SEQ ID NO 7; 25pp; English.  
 PS  
 CC The invention relates to a composition for delivering an RNA to a  
 CC mammalian cell comprising a post-synthetically modified RNA. Modifying  
 CC the RNA in the process cited above consists of covalently linking a  
 CC functional group to a ribose 2' hydroxyl of the RNA. The functional group  
 CC is selected from a hydrophobic group, membrane active compound, cell-  
 CC penetrating compound, cell-targeting signal, interaction modifier, and  
 CC steric stabiliser. The modified RNA is complexed with a transfection  
 CC agent. Modifying the RNA also increases interaction of the RNA with the  
 CC transfection agent and increases resistance of the RNA to degradation by  
 CC nucleases. The RNA is siRNA or microRNA. The methods and compositions of  
 CC the present invention are useful for the delivery of oligonucleotides and  
 CC small RNAs to cells in vitro and in vivo. The present sequence is  
 CC Bacteriophage T7 cholesterol modified cell targeting peptide MC1054 used  
 CC in an exemplification of the invention.  
 XX  
 SQ Sequence 33 AA;  
 Query Match 98.3%; Score 173; DB 8; Length 33;  
 Best Local Similarity 97.0%; Pred. No. 2e-18;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 DB |||||||||||||||||||||||||||||||||||  
 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 RESULT 12  
 ADJ46302  
 ID ADJ46302 standard; peptide; 33 AA.  
 AC ADJ46302;  
 DT 06-MAY-2004 (first entry)  
 XX T7 phase p17 protein ligand-related peptide, SEQ ID 25.  
 DE Hepatocyte delivery; T7; p17 rod domain.  
 KW Enterobacteria phage T7.  
 OS Synthetic.  
 XX  
 FH Key. Location/Qualifiers  
 FT Misc-difference 26  
 FT /note= "Wild-type residue replaced with Glu"  
 XX  
 PN WO2004013307-A2.  
 PD 12-FEB-2004.  
 XX  
 PF 04-AUG-2003; 2003WO-US024516.  
 PR 05-AUG-2002; 2002US-0401167P.  
 PR 04-AUG-2003; 2003US-00633808.  
 XX  
 PA (MIRU-) MIRUS CORP.  
 XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
 PI Wakefield D, Sebestyen MG;  
 PI WPI; 2004-203636/19.  
 DR  
 XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 XX compound.  
 PS Disclosure; Page 10; 56pp; English.  
 CC The present invention relates to a composition (I) for delivering a  
 CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
 CC compound. In (I), the compound comprises a drug (interferon). (I)  
 CC provides better hepatocyte specificity and potentially utilizes different  
 CC cellular internalization pathways which allows more flexibility in  
 CC designing delivery strategies and is useful for delivering therapeutic  
 CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
 CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
 CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
 CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
 CC changes which do disrupt hepatocyte targeting.

XX  
 PT Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 PT a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 PT compound.  
 XX  
 PS Disclosure; Page 10; 56pp; English.  
 XX  
 CC The present invention relates to a composition (I) for delivering a  
 CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
 CC compound. In (I), the compound comprises a drug (interferon). (I)  
 CC provides better hepatocyte specificity and potentially utilizes different  
 CC cellular internalization pathways which allows more flexibility in  
 CC designing delivery strategies and is useful for delivering therapeutic  
 CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
 CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
 CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
 CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
 CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
 CC changes which do disrupt hepatocyte targeting.  
 XX  
 SQ Sequence 33 AA;  
 Query Match 97.7%; Score 172; DB 8; Length 33;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-18;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 DB |||||||||||||||||||||||||||||||||||  
 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
 RESULT 13  
 ADJ46299  
 ID ADJ46299 standard; peptide; 33 AA.  
 AC ADJ46299;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX T7 phase p17 protein ligand, SEQ ID 22.  
 DE Hepatocyte delivery; T7; p17 rod domain.  
 KW Enterobacteria phage T7.  
 OS Synthetic.  
 XX  
 FH Key. Location/Qualifiers  
 FT Misc-difference 26  
 FT /note= "Wild-type residue replaced with dimethyl lysine"  
 XX  
 PN WO2004013307-A2.  
 PD 12-FEB-2004.  
 XX  
 PF 04-AUG-2003; 2003WO-US024516.  
 PR 05-AUG-2002; 2002US-0401167P.  
 PR 04-AUG-2003; 2003US-00633808.  
 XX  
 PA (MIRU-) MIRUS CORP.  
 XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
 PI Wakefield D, Sebestyen MG;  
 PI WPI; 2004-203636/19.  
 DR  
 XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
 XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
 XX compound.  
 PS Disclosure; Page 10; 56pp; English.  
 CC The present invention relates to a composition (I) for delivering a

CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
CC compound. In (I), the compound comprises a drug (interferon). (I)  
CC provides better hepatocyte specificity and potentially utilizes different  
CC cellular internalization pathways which allows more flexibility in  
CC designing delivery strategies and is useful for delivering therapeutic  
CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
CC changes which do disrupt hepatocyte targeting.  
XX  
SQ Sequence 33 AA;

Query Match 96.6%; Score 170; DB 8; Length 33;  
Best Local Similarity 97.0%; Pred. No. 5.6e-18;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 14  
ADJ46300  
ID ADJ46300 standard; peptide; 33 AA.

XX AC ADJ46300;

DT 06-MAY-2004 (first entry)

DE T7 phase p17 protein ligand, SEQ ID 23.

KW Hepatocyte delivery; T7; p17 rod domain.

XX OS Enterobacteria phage T7.

OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Misc-difference 26

FT /note= "Wild-type residue replaced with Ornithine"

XX PN WO2004013307-A2.

XX PD 12-FEB-2004.

XX PF 04-AUG-2003; 2003WO-US024516.

XX PR 05-AUG-2002; 2002US-0401167P.

XX PR 04-AUG-2003; 2003US-00633808.

XX PA (MIRU-) MIRUS CORP.

XX PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

XX PI Wakefield D, Sebestyen MG;

XX DR WPI; 2004-203636/19.

XX PT Composition useful for delivering a therapeutic cargo to a hepatocyte in  
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XX PS Disclosure; Page 10; 56pp; English.

XX The present invention relates to a composition (I) for delivering a  
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CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein

CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
CC changes which do disrupt hepatocyte targeting.

XX SQ Sequence 33 AA;

Query Match 96.6%; Score 170; DB 8; Length 33;

Best Local Similarity 97.0%; Pred. No. 5.6e-18;

Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 15

ADJ46304

ID ADJ46304 standard; peptide; 33 AA.

XX AC ADJ46304;

XX DT 06-MAY-2004 (first entry)

DE T7 phase p17 protein ligand-related peptide, SEQ ID 27.

KW Hepatocyte delivery; T7; p17 rod domain.

XX OS Enterobacteria phage T7.

OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Misc-difference 12

FT /note= "Wild-type residue replaced with Arg"

FT FT Misc-difference 19

FT /note= "Wild-type residue replaced with Arg"

FT FT Misc-difference 26

FT /note= "Wild-type residue replaced with Arg"

XX PN WO2004013307-A2.

XX PD 12-FEB-2004.

XX PF 04-AUG-2003; 2003WO-US024516.

XX PR 05-AUG-2002; 2002US-0401167P.

XX PR 04-AUG-2003; 2003US-00633808.

XX PA (MIRU-) MIRUS CORP.

XX PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

XX PI Wakefield D, Sebestyen MG;

XX DR WPI; 2004-203636/19.

XX PT Composition useful for delivering a therapeutic cargo to a hepatocyte in  
XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
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XX PS Disclosure; Page 10; 56pp; English.

XX The present invention relates to a composition (I) for delivering a  
CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
CC compound. In (I), the compound comprises a drug (interferon). (I)  
CC provides better hepatocyte specificity and potentially utilizes different  
CC cellular internalization pathways which allows more flexibility in  
CC designing delivery strategies and is useful for delivering therapeutic  
CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
CC changes which do disrupt hepatocyte targeting.

SQ Sequence 33 AA;

Query Match 94.9%; Score 167; DB 8; Length 33;  
 Best Local Similarity 90.9%; Pred. No. 1.6e-17;  
 Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSNATNTKQWRDETKGFRDEAKRFPKNTAG 33  
 |||||||:|||||:|||||:|||||:|||||  
 Db 1 KNESSNATNTKQWRDETKGFRDEAKRFPKNTAG 33

Search completed: March 30, 2005, 14:33:50  
 Job time : 171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:15:25 ; Search time 189 Seconds  
(without alignments)  
89.411 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESTNATNTKQWRDETKGFRDEAKRPNKTAG 33

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	100.0	553	1 VTFF BPT7	P03748 bacterioph
2	176	100.0	553	2 Q8LTX6	Q8LTX6 bacterioph
3	170	96.6	553	2 Q6WY17	Q6WY17 bacterioph
4	170	96.6	553	2 Q6WY69	Q6WY69 bacterioph
5	168	95.5	553	2 Q6WYC3	Q6WYC3 bacterioph
6	168	95.5	553	2 Q6WYH2	Q6WYH2 bacterioph
7	166	94.3	553	2 Q8LTX0	Q8LTX0 bacterioph
8	164	93.2	553	2 Q8LTX1	Q8LTX1 bacterioph
9	159	90.3	553	2 Q8LTX3	Q8LTX3 bacterioph
10	157	89.2	553	2 Q8LTX7	Q8LTX7 bacterioph
11	157	89.2	553	2 Q8LTX9	Q8LTX9 bacterioph
12	152	86.4	553	2 Q8LTX5	Q8LTX5 bacterioph
13	152	86.4	553	2 Q8LTX7	Q8LTX7 bacterioph
14	152	86.4	553	2 Q8LTX8	Q8LTX8 bacterioph
15	152	86.4	553	2 Q8LTX7	Q8LTX7 bacterioph
16	152	86.4	553	2 Q8LTX1	Q8LTX1 bacterioph
17	152	86.4	553	2 Q8LTX2	Q8LTX2 bacterioph
18	151	85.8	553	2 Q8LTX9	Q8LTX9 bacterioph
19	151	85.8	553	2 Q8LTX8	Q8LTX8 bacterioph
20	151	85.8	553	2 Q8LTX3	Q8LTX3 bacterioph
21	151	85.8	553	2 Q8LTX4	Q8LTX4 bacterioph
22	151	85.8	553	2 Q8LTX5	Q8LTX5 bacterioph
23	151	85.8	553	2 Q8LTX8	Q8LTX8 bacterioph
24	147	83.5	553	2 Q8LTX9	Q8LTX9 bacterioph
25	147	83.5	553	2 Q8LTX0	Q8LTX0 bacterioph
26	146	83.0	553	2 Q8LTX4	Q8LTX4 bacterioph
27	146	83.0	553	2 Q8LTX0	Q8LTX0 bacterioph
28	146	83.0	557	1 VTFF BPT3	P10308 bacterioph
29	146	83.0	558	2 Q8W5T8	Q8W5T8 bacterioph
30	146	83.0	558	2 Q8S8J8	Q8S8J8 yersinia pe
31	144	81.8	553	2 Q8LTX2	Q8LTX2 bacterioph

32	143	81.2	553	2 Q8LTX6	Q8LTX6 bacterioph
33	143	81.2	553	2 Q8LTX2	Q8LTX2 bacterioph
34	67	38.1	1647	2 Q7RRX4	Q7RRX4 plasmodium
35	61	34.7	879	2 Q41010	Q41010 pium sativ
36	61	34.7	879	2 Q7DLK2	Q7DLK2 pium sativ
37	61	34.7	1469	2 Q9LXK1	Q9LXK1 pium sativ
38	60	34.1	604	2 Q8A3N2	Q8A3N2 bacteroides
39	60	34.1	1292	2 Q9LDN0	Q9LDN0 arabidopsis
40	60	34.1	1662	2 Q23274	Q23274 arabidopsis
41	57	32.4	186	2 Q8LYL6	Q8LYL6 anabaena sp
42	57	32.4	509	2 Q8YKZ2	Q8YKZ2 anabaena sp
43	56.5	32.1	1097	2 Q13592	Q13592 saccharomyc
44	56	31.8	1785	2 Q6FS79	Q6FS79 candida glia
45	55.5	31.5	552	2 Q8ID98	Q8ID98 plasmodium

#### ALIGNMENTS

##### RESULT 1

VTFF BPT7

ID VTFF BPT7 STANDARD; PRT; 553 AA.

AC P03748;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tail fiber protein.

GN Name=17;

OS Bacteriophage T7.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;

OC T7-like viruses.

OX NCBI\_TaxID=10760;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83241725; PubMed=6864790;

RA Dunn J.J., Studier F.W.;

RT "Complete nucleotide sequence of bacteriophage T7 DNA and the

RT locations of T7 genetic elements.";

RL J. Mol. Biol. 166:477-535(1983).

CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; V01146; CAA24435.1; -.

DR PIR; A04373; TLBPF7.

DR InterPro; IPR005604; T7 tail fibre.

DR Pfam; PF03906; Phage\_T7\_tail\_1.

KW Fiber protein.

SQ SEQUENCE 553 AA; 61572 MW; 98B82DFADBDEAC1 CRC64;

Query Match 100.0%; Score 176; DB 1; Length 553;

Best Local Similarity 100.0%; Pred. No. 1.3e-15;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy : 1 KNESTNATNTKQWRDETKGFRDEAKRPNKTAG 33

Db : 186 KNESTNATNTKQWRDETKGFRDEAKRPNKTAG 218

##### RESULT 2

Q8LTX6

ID Q8LTX6 PRELIMINARY; PRT; 553 AA.

AC Q8LTX6;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Tail fiber protein.

GN Name=17.0;

OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an  
RL experimental lineage of bacteriophage T7.";  
DR EMBL; AF419438; AAM43534.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage\_T7\_tail; 1.  
SQ SEQUENCE 553 AA; 61560 MW; 11A394FADBDBEAD1 CRC64;

Query Match 100.0%; Score 176; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.3e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

## RESULT 3

Q6WY17 PRELIMINARY; PRT; 553 AA.  
AC Q6WY17;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Gene 17.  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22990536; PubMed=14629033;  
RA Bull J.J., Badgett M.R., Rokytá D., Molineux I.J.;  
RT "Experimental evolution yields hundreds of mutations in a functional  
RT viral genome.";  
RL J. Mol. Evol. 57:241-248(2003).  
DR EMBL; AY264778; AAP34164.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage\_T7\_tail; 1.  
SQ SEQUENCE 553 AA; 61833 MW; ECF0426C8E74CC13 CRC64;

Query Match 96.6%; Score 170; DB 2; Length 553;  
Best Local Similarity 97.0%; Pred. No. 8.8e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

## RESULT 4

Q6WY69 PRELIMINARY; PRT; 553 AA.  
AC Q6WY69;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Gene 17.  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22990536; PubMed=14629033;

RA Bull J.J., Badgett M.R., Rokytá D., Molineux I.J.;  
RT "Experimental evolution yields hundreds of mutations in a functional  
RT viral genome.";  
RL J. Mol. Evol. 57:241-248(2003).  
DR EMBL; AY264777; AAP34112.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage\_T7\_tail; 1.  
SQ SEQUENCE 553 AA; 61787 MW; 58F0426D9A74CC11 CRC64;

Query Match 96.6%; Score 170; DB 2; Length 553;  
Best Local Similarity 97.0%; Pred. No. 8.8e-15;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

## RESULT 5

Q6WYC3 PRELIMINARY; PRT; 553 AA.  
AC Q6WYC3;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Gene 17.  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22990536; PubMed=14629033;  
RA Bull J.J., Badgett M.R., Rokytá D., Molineux I.J.;  
RT "Experimental evolution yields hundreds of mutations in a functional  
RT viral genome.";  
RL J. Mol. Evol. 57:241-248(2003).  
DR EMBL; AY264776; AAP34058.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage\_T7\_tail; 1.  
SQ SEQUENCE 553 AA; 61788 MW; 8E754373B814980C CRC64;

Query Match 95.5%; Score 168; DB 2; Length 553;  
Best Local Similarity 97.0%; Pred. No. 1.7e-14;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

## RESULT 6

Q6WYH2 PRELIMINARY; PRT; 553 AA.  
AC Q6WYH2;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Gene 17.  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22990536; PubMed=14629033;  
RA Bull J.J., Badgett M.R., Rokytá D., Molineux I.J.;  
RT "Experimental evolution yields hundreds of mutations in a functional  
RT viral genome.";  
RL J. Mol. Evol. 57:241-248(2003).  
DR EMBL; AY264775; AAP34009.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage\_T7\_tail; 1.



SQ SEQUENCE 553 AA; 61832 MW; CE2632DB5E3B85F CRC64;  
Query Match 95.5%; Score 168; DB 2; Length 553;  
Best Local Similarity 97.0%; Pred. No. 1.7e-14;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33  
|||||  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 218  
|||||

RESULT 7  
QBLTX0 PRELIMINARY; PRT; 553 AA.  
AC QBLTX0;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an  
RT experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419444; AAM43540.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 61829 MW; 8B95AA3956CDEE9 CRC64;

Query Match 94.3%; Score 166; DB 2; Length 553;  
Best Local Similarity 96.9%; Pred. No. 3.1e-14;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217  
|||||

RESULT 8  
QBLTX1 PRELIMINARY; PRT; 553 AA.  
AC QBLTX1;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an  
RT experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419443; AAM43539.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 61753 MW; ADAB0C4B2E5BDB16 CRC64;

Query Match 93.2%; Score 164; DB 2; Length 553;  
Best Local Similarity 96.9%; Pred. No. 5.9e-14;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217  
|||||

RESULT 9  
QBLTU3 PRELIMINARY; PRT; 553 AA.  
AC QBLTU3;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an  
RT experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419510; AAM43606.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 62081 MW; E32BB0B02ADAF22 CRC64;

Query Match 90.3%; Score 159; DB 2; Length 553;  
Best Local Similarity 93.8%; Pred. No. 2.9e-13;  
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217  
|||||

RESULT 10  
QBLTW7 PRELIMINARY; PRT; 553 AA.  
AC QBLTW7;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an  
RT experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419447; AAM43543.1; -  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 61952 MW; FDBF4FB200825A99 CRC64;

Query Match 89.2%; Score 157; DB 2; Length 553;  
Best Local Similarity 93.8%; Pred. No. 5.4e-13;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
Db 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217  
|||||

```
RESULT 11
Q8LTW9
ID Q8LTW9 PRELIMINARY; PRT; 553 AA.
AC Q8LTW9;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419445; AAM43541.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61805 MW; 882675FB6B09895F CRC64;

Query Match 89.2%; Score 157; DB 2; Length 553;
Best Local Similarity 93.8%; Pred. No. 5.4e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKTA 32
Db 186 KNESSTNATNTKQWRDEIKDFRDEAKRPNKTA 217

RESULT 12
Q8LTU5
ID Q8LTU5 PRELIMINARY; PRT; 553 AA.
AC Q8LTU5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419508; AAM43604.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 62184 MW; 66A0BC1246E4E421 CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;
Best Local Similarity 90.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKTA 32
Db 186 KNESSTNATNTKQWRDEIKDFRDEAKRPNKTA 217

RESULT 13
Q8LTU7
ID Q8LTU7 PRELIMINARY; PRT; 553 AA.
AC Q8LTU7;
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DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419506; AAM43602.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 62092 MW; E0E509A5FAADA3EC CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;
Best Local Similarity 90.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKTA 32
Db 186 KNESSTNATNTKQWRDEIKDFRDEAKRPNKTA 217

RESULT 14
Q8LTU8
ID Q8LTU8 PRELIMINARY; PRT; 553 AA.
AC Q8LTU8;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419505; AAM43601.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 62303 MW; 5868AAE51F700C CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;
Best Local Similarity 90.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKTA 32
Db 186 KNESSTNATNTKQWRDEIKDFRDEAKRPNKTA 217

RESULT 15
Q8LTXT7
ID Q8LTXT7 PRELIMINARY; PRT; 553 AA.
AC Q8LTXT7;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
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OS Bacteriophage T7.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
 OC T7-like viruses.  
 OX NCBI\_TaxID=10760;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22013848; PubMed=12019219;  
 RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
 RT "Distinguishing between selection and population expansion in an  
 RT experimental lineage of bacteriophage T7";  
 RL Genetics 161:11-20(2002).  
 DR EMBL; AF419437; AA043533.1; -  
 DR InterPro; IPR005604; T7\_tail\_fibre.  
 DR Pfam; PF03906; Phage\_T7\_tail; 1.  
 SQ SEQUENCE 553 AA; 62029 MW; 88C653CDF5C4FEB9 CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;  
 Best Local Similarity 90.6%; Pred. No. 2.6e-12;  
 Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTA 32  
 Db 186 KDESSTNATNTKQWRDEIKDFRDEAKRPFKNTA 217

Search completed: March 30, 2005, 14:37:06  
 Job time : 190 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 14:27:07 ; Search time 43 Seconds  
(without alignments)  
73.841 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESSTATNTKQWRDETKGFRDEAKRPKNTAG 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	100.0	553	1 TLBP7	tail fiber protein
2	146	83.0	557	1 TLBP73	tail fiber protein
3	61	34.7	879	2 S49910	chloroplast outer
4	60	34.1	1662	1 H71402	probable kinesin -
5	57	32.4	186	2 A2450	hypothetical prote
6	57	32.4	509	2 A2496	transposase alr714
7	56.5	32.1	3079	1 RGBY12	probable GTPase-ac
8	55	31.2	466	2 T07404	probable glucosylt
9	54	30.7	346	2 G87440	rod shape-determ
10	53	30.1	167	2 S46656	ubiquitin-protein
11	53	30.1	880	2 T48477	hypothetical prote
12	52	29.5	69	2 A82489	cold shock DNA-bin
13	52	29.5	169	2 T02943	ubiquitin-conjugat
14	51.5	29.3	174	2 A26666	conserved hypotet
15	51.5	29.3	192	2 B97448	immunoreactive 14K
16	51	29.0	166	2 S71209	ubiquitin-protein
17	51	29.0	573	2 F81313	peptidase (M3 fami
18	50.5	28.7	648	2 A83792	acetyl-CoA synthet
19	50	28.4	136	2 A96905	uncharacterized sm
20	50	28.4	476	2 T03745	glucosyltransferas
21	50	28.4	751	2 B87391	TonB-dependent rec
22	50	28.4	960	2 AF1940	isoleucyl-tRNA syn
23	50	28.4	2481	2 D90011	FmtB protein [impo
24	50	28.4	3328	2 T30835	breast cancer tumo
25	50	28.4	3329	2 T42205	breast cancer susc
26	50	28.4	3329	2 T30904	breast cancer tumo
27	49	27.8	70	2 E82399	cold shock domain
28	49	27.8	298	2 S50735	hypothetical prote
29	49	27.8	336	2 G81152	probable DNA-bind

#### ALIGNMENTS

##### RESULT 1

TLBP7

tail fiber protein - phase T7

C:Species: phase T7

C:Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A04373; S42333

R:Dunn, J.J.; Thompson, K.

submitted to the Nucleic Acid Sequence Database, September 1982

A:Reference number: A94615

A:Accession: A04373

A:Molecule type: DNA

A:Residues: 1-553 <DUN>

A:Cross-references: UNIPROT:P03748

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 166, 477-535, 1983

A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 gene

A:Reference number: S42283; MUID:83241725; PMID:6864790

A:Accession: S42333

A:Molecule type: DNA

A:Residues: 1-553 <DUN>

A:Cross-references: EMBL:V01146; NID:9431187; PIDN:CAA24435.1; PID:gl5611

A:Note: the authors did not translate the codon for residue 1

C:Genetics:

A:Gene: 17

A:Map position: 86.70-90.85

C:Superfamily: phase T7 tail fiber protein

C:Keywords: tail fiber

Query Match 100.0%; Score 176; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 7.5e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTATNTKQWRDETKGFRDEAKRPKNTAG 33

|||||

Db 186 KNESSTATNTKQWRDETKGFRDEAKRPKNTAG 218

##### RESULT 2

TLBP73

tail fiber protein - phase T3

C:Species: phase T3

A:Note: host Escherichia coli

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C:Accession: A23476

R:Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, T.

Virology 151, 350-361, 1986

A:Title: Cloning and sequencing of the genetic right end of bacteriophage T3 DNA.

A:Reference number: A94339; MUID:86209997; PMID:3010556

A:Accession: A23476

A:Molecule type: DNA

A:Residues: 1-557 <YAM>

A:Cross-references: UNIPROT:P10308; GB:M14784; NID:g215810; PIDN:AAA92523.1; PID:g215811

mitochondrial inne  
hypothetical prote  
hypothetical prote  
probable DNA ligas  
hypothetical prote  
hypothetical prote  
conserved hypotet  
centromere protein  
hypothetical prote  
glucosyltransferas  
hypothetical prote  
hypothetical prote  
surface antigen - P  
desmoplakin I - hu  
fibrinogen alpha-I  
voltage-dependent  
ubiquitin-protein

30 49 27.8 453 2 JE0155  
31 49 27.8 615 2 T06108  
32 48.5 27.6 112 2 T06732  
33 48.5 27.6 282 2 B81264  
34 48.5 27.6 604 2 A84753  
35 48.5 27.6 774 2 A10106  
36 48.5 27.6 2663 1 S28261  
37 48 27.3 210 2 T06656  
38 48 27.3 476 2 T03747  
39 48 27.3 549 2 T40692  
40 48 27.3 1222 2 G59100  
41 48 27.3 2543 2 T31687  
42 48 27.3 2677 2 A38194  
43 47.5 27.0 641 1 A41932  
44 47.5 27.0 2206 2 JC5280  
45 47 26.7 166 2 T45703



ubiquitin-protein ligase [EC 6.3.2.19] UBC14 [similarity] - Arabidopsis thaliana  
N;Alternate names: ubiquitin carrier protein E2 (clone RAY029) ; ubiquitin-conjugating e;  
C;Species: Arabidopsis thaliana (mouse-ear cress)

RESULT 12

A82489  
cold shock DNA-binding domain protein VCA0184 [imported] - Vibrio cholerae (strain N1696)  
C/Species: Vibrio cholerae  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: A82489  
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.;  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A/Reference number: A82035; MUID:20406833; PMID:10952301  
A/Accession: A82489  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-69 <HEI>  
A/Cross-references: UNIPROT:O9KMY2; GB:AE004359; GB:AE003853; NID:g9657575; PIDN:AAF9609  
A/Experimental source: serogroup O1; strain N16961; biotype El Tor  
C/Genetics:  
A/Gene: VCA0184  
A/Map position: 2  
C/Superfamily: cold shock protein, cspA type; cold shock domain homology

Query Match	29.5%	Score 52	DB 2	Length 69
Best Local Similarity	58.8%	Pred. No. 3.7		
Matches	10; Conservative	2; Mismatches	5; Indels	0; Gaps

Qy 5 STNATNTKQWRDETKGF 21  
||| ||| : ||| |||  
Db 2 STPVTGTVKWFNETKGF 18

RESULT 13

T02943  
ubiquitin-conjugating enzyme - maize  
N/Alternate names: ubiquitin carrier protein  
C/Species: Zea mays (maize)  
C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C/Accession: T02943  
R/de Vries, A.; Cordts, S.; Dresselhaus, T.  
Plant Physiol. 118, 1101, 1998  
A/Title: Molecular Characterization of a cDNA Encoding an Ubiquitin Carrier Protein (UBC)  
A/Reference number: Z14787; MUID:99105148; PMID:9890811  
A/Accession: T02943  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-169 <DEV>  
A/Cross-references: UNIPROT:Q24560; EMBL:AJ002959; PIDN:CAA05772.1  
C/Superfamily: human ubiquitin-protein ligase E2

Query Match	29.5%	Score 52	DB 2	Length 169
Best Local Similarity <td>30.8%</td> <td>Pred. No. 9.7</td> <td></td> <td></td>	30.8%	Pred. No. 9.7		
Matches	8; Conservative	8; Mismatches	10; Indels	0; Gaps

Qy 2 NESSTNATNTKQWRDETKGRDEAKR 27  
: || | : ||| : ||| : : :  
Db 135 DESPANTEAKEWRQREDFKKKVR 160

RESULT 14

AD2666  
conserved hypothetical protein Atu0730 [imported] - Agrobacterium tumefaciens (strain C5)  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AD2666  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan,  
Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.



Search completed: March 30, 2005, 14:38:05  
Job time : 54 secs

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